OIPE

RAW SEQUENCE LISTING   DATE: 09/18/2001
PATENT APPLICATION: US/09/938,641   TIME: 11:13:51

Input Set : A:\211226US0X.txt
Output Set: N:\CRF3\09182001\I938641.raw

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 3  <110> APPLICANT: MARX, ACHIM
 4         FARWICK, MIKE
 5         HERMANN, THOMAS
 6         SCHISCHKA, NATALIE
 7         BATHE, BRIGITTE
 9  <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE oxyR GENE
11  <130> FILE REFERENCE: 211226US0X
13  <140> CURRENT APPLICATION NUMBER: US/09/938,641
13  <141> CURRENT FILING DATE: 2001-08-27
13  <150> PRIOR APPLICATION NUMBER: DE 10042052.4
14  <151> PRIOR FILING DATE: 2000-08-26
16  <150> PRIOR APPLICATION NUMBER: DE 10110053.1
17  <151> PRIOR FILING DATE: 2001-03-02
19  <150> PRIOR APPLICATION NUMBER: US 60/279,415
20  <151> PRIOR FILING DATE: 2001-03-29
22  <160> NUMBER OF SEQ ID NOS: 4
24  <170> SOFTWARE: PatentIn version 3.1
26  <210> SEQ ID NO: 1
27  <211> LENGTH: 1675
28  <212> TYPE: DNA
29  <213> ORGANISM: Corynebacterium glutamicum
31  <220> FEATURE:
32  <221> NAME/KEY: CDS
33  <222> LOCATION: (491)..(1471)
34  <223> OTHER INFORMATION:
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38  gccaaccgca gggcatttac catcatggtg cgcaacgcca tgttccgcct tgtggagcta     60
40  tttgcttatg aaaaggaaga tcagcttagt cagatgactg aatacctgga tgaggctcct    120
42  gatttcggtg ctgcgatgga tgcgtacttt gatgaatatg cggatcttga taccggcccg    180
44  gcagctcgtg gaccagagtt cttcaaggta gagcacacgg gaagaatgtg ggaggtgcgt    240
46  caggtggtga aggatccaga aggtgataat tccttcgcgt ttgttgccac cattgatctt    300
48  gatgcctctg atgatgcagg tgaggtgcgt tttggatcgc tgtcgattga ccacaactag    360
50  gggtttgcgt cgaaaagcaa gcacgcctgg tgcctgattt gagcggtttt acctatggcg    420
52  ctttggcgcc gtcaaactgt cccagcgatt tcattattat tttcgtgcat tcaccgttat    480
54  agttataggc atg agc aat aaa gag tac cgg ccc aca ctc gcc cag ctt       529
55              Met Ser Asn Lys Glu Tyr Arg Pro Thr Leu Ala Gln Leu
56               1               5                  10
58  cgc acc ttt gtc acc atc gca gaa tgc aag cac ttt ggt act gct gcc     577
59  Arg Thr Phe Val Thr Ile Ala Glu Cys Lys His Phe Gly Thr Ala Ala
60      15                  20                  25
62  acc aag ctg tcc att tcg cag cca tcc ctc tcc cag gca ctt gtc gca     625
63  Thr Lys Leu Ser Ile Ser Gln Pro Ser Leu Ser Gln Ala Leu Val Ala
64  30                  35                  40                  45
66  tta gaa aca ggc ctg gga gtt cag ctg att gaa cgc tcc acc cgc aag     673
67  Leu Glu Thr Gly Leu Gly Val Gln Leu Ile Glu Arg Ser Thr Arg Lys
68                  50                  55                  60
70  gtc att gtc acc cca gcg ggc gag aag ttg ctg cca ttc gcc aaa tcc     721
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71 Val Ile Val Thr Pro Ala Gly Glu Lys Leu Leu Pro Phe Ala Lys Ser
72              65                  70                  75
74 acc ctt gac gcg gcg gag tct ttc ctc tcc cac gcc aag ggc gcc aac      769
75 Thr Leu Asp Ala Ala Glu Ser Phe Leu Ser His Ala Lys Gly Ala Asn
76              80                  85                  90
78 ggt tcg ctc act gga ccg ttg acc gta ggc atc atc ccc acg gcg gct      817
79 Gly Ser Leu Thr Gly Pro Leu Thr Val Gly Ile Ile Pro Thr Ala Ala
80          95                  100                 105
82 cct tac att ttg ccg tca atg ctg tcc atc gtg gat gaa gaa tat cca      865
83 Pro Tyr Ile Leu Pro Ser Met Leu Ser Ile Val Asp Glu Glu Tyr Pro
84 110                 115                 120                 125
86 gat ctg gaa cct cac atc gtc gag gac caa acc aag cat ctt ctc gcg      913
87 Asp Leu Glu Pro His Ile Val Glu Asp Gln Thr Lys His Leu Leu Ala
88                  130                 135                 .140
90 ttg ctg cgc gac ggc gcc atc gac gtc gcc atg atg gcc ctg cct tct      961
91 Leu Leu Arg Asp Gly Ala Ile Asp Val Ala Met Met Ala Leu Pro Ser
92              145                 150                 155
94 gag gca cca ggc atg aag gaa atc ccc ctc tac gac gaa gac ttt atc      1009
95 Glu Ala Pro Gly Met Lys Glu Ile Pro Leu Tyr Asp Glu Asp Phe Ile
96          160                 165                 170
98 gtc gtt aca gct agc gat cac ccc ttc gcc ggc cgc caa gac tta gaa      1057
99 Val Val Thr Ala Ser Asp His Pro Phe Ala Gly Arg Gln Asp Leu Glu -
100     175                 180                 185
102 cta tcc gcc tta gaa gac ctc gat ctg ctg ctt ctc gac gac gga cac     1105
103 Leu Ser Ala Leu Glu Asp Leu Asp Leu Leu Leu Leu Asp Asp Gly His
104 190                 195                 200                 205
106 tgc ctc cac gac caa att gtg gac ctg tgc cgc cgc gga gac atc aac     1153
107 Cys Leu His Asp Gln Ile Val Asp Leu Cys Arg Arg Gly Asp Ile Asn
108                 210                 215                 220
110 ccc att agc tcc act act gct gtc acc cgc gca tcc agc ctt acc acc     1201
111 Pro Ile Ser Ser Thr Thr Ala Val Thr Arg Ala Ser Ser Leu Thr Thr
112             225                 230                 235
114 gtc atg cag ctc gtc gtc gcc ggc ctt gga tcc acc ttg gtc cca atc     1249
115 Val Met Gln Leu Val Val Ala Gly Leu Gly Ser Thr Leu Val Pro Ile
116         240                 245                 250
118 agc gca atc cca tgg gaa tgc acc cga cca gga ctg gca aca gcc aac     1297
119 Ser Ala Ile Pro Trp Glu Cys Thr Arg Pro Gly Leu Ala Thr Ala Asn
120     255                 260                 265
122 ttc aac tct gat gtc acc gca aac cgc cgc att gga ttg gtg tac cgt     1345
123 Phe Asn Ser Asp Val Thr Ala Asn Arg Arg Ile Gly Leu Val Tyr Arg
124 270                 275                 280                 285
126 tcc tct tct tct cgc gcc gaa gag ttc gaa cag ttt gca ctc att ttg     1393
127 Ser Ser Ser Ser Arg Ala Glu Glu Phe Glu Gln Phe Ala Leu Ile Leu
128                 290                 295                 300
130 cag cgc gct ttc caa gaa gcc gtc gcg ctt gct gcc tca act ggc atc     1441
131 Gln Arg Ala Phe Gln Glu Ala Val Ala Leu Ala Ala Ser Thr Gly Ile
132             305                 310                 315
134 acc ttg aag caa aat gtc gcg gta gcg cag taagtttttc tagaggtttt       1491
135 Thr Leu Lys Gln Asn Val Ala Val Ala Gln
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136         320                325
138 ccagagtcag ctacaagcaa aaagcccttt ccattgatgc acaccaacgt gagattcaag   1551
140 ggaaagggct ttattgattg cagaatgcct actgcattag cggcgctcca ccggaatatt   1611
142 tccaccactg atctggcggt aaatatgaac ggtagacagc atcattactg gcagcacgat   1671
144 gatc                                                                1675
147 <210> SEQ ID NO: 2
148 <211> LENGTH: 327
149 <212> TYPE: PRT
150 <213> ORGANISM: Corynebacterium glutamicum
152 <400> SEQUENCE: 2
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155 1               5                   10                  15
158 Val Thr Ile Ala Glu Cys Lys His Phe Gly Thr Ala Ala Thr Lys Leu
159             20                  25                  30
162 Ser Ile Ser Gln Pro Ser Leu Ser Gln Ala Leu Val Ala Leu Glu Thr
163             35                  40                  45
166 Gly Leu Gly Val Gln Leu Ile Glu Arg Ser Thr Arg Lys Val Ile Val
167     50                  55                  60
170 Thr Pro Ala Gly Glu Lys Leu Leu Pro Phe Ala Lys Ser Thr Leu Asp
171 65                  70                  75                  80
174 Ala Ala Glu Ser Phe Leu Ser His Ala Lys Gly Ala Asn Gly Ser Leu
175             85                  90                  95
178 Thr Gly Pro Leu Thr Val Gly Ile Ile Pro Thr Ala Ala Pro Tyr Ile
179             100                 105                 110
182 Leu Pro Ser Met Leu Ser Ile Val Asp Glu Glu Tyr Pro Asp Leu Glu
183             115                 120                 125
186 Pro His Ile Val Glu Asp Gln Thr Lys His Leu Leu Ala Leu Leu Arg
187     130                 135                 140
190 Asp Gly Ala Ile Asp Val Ala Met Met Ala Leu Pro Ser Glu Ala Pro
191 145                 150                 155                 160
194 Gly Met Lys Glu Ile Pro Leu Tyr Asp Glu Asp Phe Ile Val Val Thr
195             165                 170                 175
198 Ala Ser Asp His Pro Phe Ala Gly Arg Gln Asp Leu Glu Leu Ser Ala
199             180                 185                 190
202 Leu Glu Asp Leu Asp Leu Leu Leu Leu Asp Asp Gly His Cys Leu His
203             195                 200                 205
206 Asp Gln Ile Val Asp Leu Cys Arg Arg Gly Asp Ile Asn Pro Ile Ser
207     210                 215                 220
210 Ser Thr Thr Ala Val Thr Arg Ala Ser Ser Leu Thr Thr Val Met Gln
211 225                 230                 235                 240
214 Leu Val Val Ala Gly Leu Gly Ser Thr Leu Val Pro Ile Ser Ala Ile
215             245                 250                 255
218 Pro Trp Glu Cys Thr Arg Pro Gly Leu Ala Thr Ala Asn Phe Asn Ser
219             260                 265                 270
222 Asp Val Thr Ala Asn Arg Arg Ile Gly Leu Val Tyr Arg Ser Ser Ser
223             275                 280                 285
226 Ser Arg Ala Glu Glu Phe Glu Gln Phe Ala Leu Ile Leu Gln Arg Ala
227     290                 295                 300
230 Phe Gln Glu Ala Val Ala Leu Ala Ala Ser Thr Gly Ile Thr Leu Lys
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234 Gln Asn Val Ala Val Ala Gln
235              325
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239 <211> LENGTH: 30
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: Synthetic DNA
246 <400> SEQUENCE: 3
247 gatcgagaat tcaaaggaag atcagcttag                              30
250 <210> SEQ ID NO: 4
251 <211> LENGTH: 20
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: Synthetic DNA
258 <400> SEQUENCE: 4
259 ggaaaacctc tagaaaaact                                         20
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VERIFICATION SUMMARY   DATE: 09/18/2001
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date